

DISPERSAL BETWEEN ISOLATED SEAMOUNT POPULATIONS - A MOLECULAR APPROACH

A final report for AASERT Award to Grant N00014-89-J-1431
For the period 01 Jun 1992 to 31 May 1996

Submitted on 14 September, 1996 to the Office of Naval Research by:

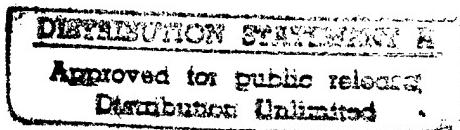
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This AASERT has supported a graduate student, Ewann Agenbroad, in her studies of population genetics, gene flow and phylogeny of seamount corals. The project was initially organized around three Pisces IV submersible cruises (operated through NOAA's Hawaiian Underwater Research Laboratory), scheduled for summers of 1993, 1994 and 1995. The 1993 cruise was completed, allowing us to collect multiple individuals of more than 20 coral species from three seamounts in the Northern Hawaiian Ridge. These initial samples allowed us to conduct pilot studies on genetic variation in the mitochondrial 16S rRNA among individuals and species from these three seamounts. Although variation within species was low in this genomic region, further studies are underway using other, more variable regions in the target species *Narella nuttingi*. The species-level variation in 16S rRNA, however, was very intriguing, and spawned a promising phylogenetic study.

The 1994 and 1995 cruises were postponed, and rescheduled for summer 1996. Because of this postponement, Ewann will be using ethanol-preserved coral specimens from the Smithsonian Institute and other museums in order to accomplish her gene flow and phylogenetic studies. Fortunately, corals have traditionally been preserved in ethanol, and Ewann has adapted an existing protocol for extracting DNA from these ethanol-preserved specimens. In addition, numerous individuals of the target species *N. nuttingi* are available in museum collections. Ewann will therefore concentrate on museum specimens, but take advantage of Pisces V collections when they become available in the future.

Ewann has completed her coursework and successfully defended her thesis proposal, "Phylogenetic relationships and species-level variation within the class Anthozoa as determined through DNA sequence analyses", to her thesis committee, which consists of myself, Dave Caron (WHOI), Paul Matsudaira (MIT), Patricia Wainwright (Rutgers) and Scott France (UNH). A summary of preliminary results (in collaboration with Scott France) are presented below.

Coral Phylogeny. The mitochondrial 16S rRNA of seamount corals shows little variation within species, but significant variation between species. This region of the genome is therefore more appropriate for phylogenetic, rather than population studies. A comparison of the 16S rRNA region among species in the Class Anthozoa showed that members of Orders Antipatharia



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Coral Gene Flow. Although the mitochondrial 16S rRNA appears not to be a suitable genomic region for population-level studies, nuclear regions, such as internally-transcribed spacers (ITS; occurring between the 18S, 5.8S and 28S rRNA genes) and microsatellites appear to be highly variable within species. Future gene flow studies will concentrate on the genetic variation of ITS regions and microsatellites in *Narella nuttingi*, a common, widespread species of seamount coral.

PUBLICATIONS SUPPORTED BY THIS GRANT:

France, S.C., P.E. Rosel, J.W. Agenbroad, L.S. Mullineaux, T.D. Kocher. 1996. DNA sequence variation of mitochondrial large-subunit rRNA provides support for a two subclass organization of the Anthozoa (Cnidaria). Molecular Marine Biology and Biotechnology 5:15-28.

PRESENTATIONS, ABSTRACTS:

Agenbroad, J.E., S.C. France, L.S. Mullineaux. 1995. Sequence variation in mitochondrial 16S rRNA of three subclasses of anthozoans (Phylum Cnidaria). Poster presented at Keystone Symposium in Santa Fe: Molecular Approaches to Marine Ecology and Evolution.

REPORT DOCUMENTATION PAGE			Form Approved OMB No. 0704-0188
<small>Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information, including suggestions for reducing this burden. To Washington Headquarters Services, Directorate for Information Operations and Reports, 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302, and to the Office of Management and Budget, Paperwork Reduction Project (0704-0188), Washington, DC 20503.</small>			
1. AGENCY USE ONLY (Leave blank)	2. REPORT DATE	3. REPORT TYPE AND DATES COVERED	
		FINAL REPORT	thru 5/31/96
4. TITLE AND SUBTITLE		5. FUNDING NUMBERS	
DISPERSAL AND RETENTION OF BENTHIC INVERTEBRATE LARVAE IN FLOWS NEAR A SEAMOUNT		N00014-89-J-1431	
6. AUTHOR(S)			
Lauren S. Mullineaux			
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)		8. PERFORMING ORGANIZATION REPORT NUMBER	
WOODS HOLE OCEANOGRAPHIC INSTITUTION WOODS HOLE, MA 02543		W.H.O.I. Proposal No. 7350.1	
9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)		10. SPONSORING/MONITORING AGENCY REPORT NUMBER	
Eric Shulenberger, Code 322BC ONR, 800 N. Quincy Street Arlington, VA 22217-5000			
11. SUPPLEMENTARY NOTES			
12a. DISTRIBUTION / AVAILABILITY STATEMENT		12b. DISTRIBUTION CODE	
13. ABSTRACT (Maximum 200 words)			
<p>The primary goals of this project were to: (1) investigate effects of mesoscale flows on retention and dispersal of benthic invertebrate larvae near seamounts, and (2) define the influences of flow-mediated dispersal on population ecology and gene flow in isolated benthic habitats. We tested the hypothesis that hydrodynamic features associated with seamounts retain larvae and cause them to accumulate near their source. To accomplish this, we first conducted experiments in the field and a laboratory flume were to develop a technique that allowed us to infer larval abundance patterns from colonization patterns on arrays of settlement plates. In a subsequent series of field collections, we showed that the distributions of invertebrate larvae in the plankton and recruits on settlement panels were consistent with a process of larval retention in tidally-rectified flows near the seamount.</p> <p>Population genetic studies were attempted by comparing the mitochondrial 16S rRNA gene of several coral species among populations on three seamount. Although this gene was not suitable for population-level studies, a broader study of anthozoan 16S rRNA proved relevant to a long-standing controversy in the phylogeny of Class Anthozoa.</p>			
14. SUBJECT TERMS		15. NUMBER OF PAGES	
		16. PRICE CODE	
17. SECURITY CLASSIFICATION OF REPORT	18. SECURITY CLASSIFICATION OF THIS PAGE	19. SECURITY CLASSIFICATION OF ABSTRACT	20. LIMITATION OF ABSTRACT

NSN 7540-01-280-5500

 Standard Form 298 (Rev. 2-89)
 Prescribed by ANSI Std. Z39-18
 298-102